

RAW SEQUENCE LISTING

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Application Serial Number: 1015681578
Source: TFWP
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/568,578

DATE: 02/01/2007
TIME: 12:16:16

Input Set : A:\02856701.APP
Output Set: N:\CRF4\02012007\J568578.raw

3 <110> APPLICANT: HIHARA, SATOSHI
4 DOI, HIROFUMI
6 <120> TITLE OF INVENTION: INTERACTION INHIBITORS, METHOD OF DETECTING INTERACTION
7 INHIBITOR AND KIT FOR DETECTING INTERACTION INHIBITOR
9 <130> FILE REFERENCE: 028567-0145
11 <140> CURRENT APPLICATION NUMBER: 10/568,578
12 <141> CURRENT FILING DATE: 2006-02-17
14 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/011686
15 <151> PRIOR FILING DATE: 2004-08-13
17 <150> PRIOR APPLICATION NUMBER: JP 2003-295204
18 <151> PRIOR FILING DATE: 2003-08-19
20 <160> NUMBER OF SEQ ID NOS: 11
22 <170> SOFTWARE: PatentIn Ver. 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 23
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
31 primer
33 <400> SEQUENCE: 1
34 atgtcgccat ttcttcggat tgg 23
37 <210> SEQ ID NO: 2
38 <211> LENGTH: 19
39 <212> TYPE: DNA
40 <213> ORGANISM: Artificial Sequence
42 <220> FEATURE:
43 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
44 primer
46 <400> SEQUENCE: 2
47 tcagtagatc agccgctcc 19
50 <210> SEQ ID NO: 3
51 <211> LENGTH: 21
52 <212> TYPE: DNA
53 <213> ORGANISM: Artificial Sequence
55 <220> FEATURE:
56 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
57 primer
59 <400> SEQUENCE: 3
60 atgaccaccc cagaaaaaga g 21
63 <210> SEQ ID NO: 4
64 <211> LENGTH: 19
65 <212> TYPE: DNA

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66 <213> ORGANISM: Artificial Sequence
 68 <220> FEATURE:
 69 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 70 primer
 72 <400> SEQUENCE: 4
 73 tcaaagctgg aaacacctcc 19
 76 <210> SEQ ID NO: 5
 77 <211> LENGTH: 35
 78 <212> TYPE: DNA
 79 <213> ORGANISM: Artificial Sequence
 81 <220> FEATURE:
 82 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 83 primer
 85 <400> SEQUENCE: 5
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 89 <210> SEQ ID NO: 6
 90 <211> LENGTH: 30
 91 <212> TYPE: DNA
 92 <213> ORGANISM: Artificial Sequence
 94 <220> FEATURE:
 95 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 96 primer
 98 <400> SEQUENCE: 6
 99 ctgcgatcac atggatccat gcttcatccc 30
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 103 <211> LENGTH: 30
 104 <212> TYPE: DNA
 105 <213> ORGANISM: Artificial Sequence
 107 <220> FEATURE:
 108 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 109 primer
 111 <400> SEQUENCE: 7
 112 gcggccgcaa tggacaaact gttccccctc 30
 115 <210> SEQ ID NO: 8
 116 <211> LENGTH: 28
 117 <212> TYPE: DNA
 118 <213> ORGANISM: Artificial Sequence
 120 <220> FEATURE:
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 122 primer
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 125 ctgcgatcac gagctgatct gactcagc 28
 128 <210> SEQ ID NO: 9
 129 <211> LENGTH: 706
 130 <212> TYPE: PRT
 131 <213> ORGANISM: Homo sapiens
 133 <400> SEQUENCE: 9
 134 Met Ser Pro Phe Leu Arg Ile Gly Leu Ser Asn Phe Asp Cys Gly Ser
 135 1 5 10 15

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137 Cys Gln Ser Cys Gln Gly Glu Ala Val Asn Pro Tyr Cys Ala Val Leu
138 20 25 30
140 Val Lys Glu Tyr Val Glu Ser Glu Asn Gly Gln Met Tyr Ile Gln Lys
141 35 40 45
143 Lys Pro Thr Met Tyr Pro Pro Trp Asp Ser Thr Phe Asp Ala His Ile
144 50 55 60
146 Asn Lys Gly Arg Val Met Gln Ile Ile Val Lys Gly Lys Asn Val Asp
147 65 70 75 80
149 Leu Ile Ser Glu Thr Thr Val Glu Leu Tyr Ser Leu Ala Glu Arg Cys
150 85 90 95
152 Arg Lys Asn Asn Gly Lys Thr Glu Ile Trp Leu Glu Leu Lys Pro Gln
153 100 105 110
155 Gly Arg Met Leu Met Asn Ala Arg Tyr Phe Leu Glu Met Ser Asp Thr
156 115 120 125
158 Lys Asp Met Asn Glu Phe Glu Thr Glu Gly Phe Phe Ala Leu His Gln
159 130 135 140
161 Arg Arg Gly Glu Ile Lys Gln Ala Lys Val His His Val Lys Cys His
162 145 150 155 160
164 Glu Phe Thr Ala Thr Phe Phe Pro Gln Pro Thr Phe Cys Ser Val Cys
165 165 170 175
167 His Glu Phe Val Trp Gly Leu Asn Lys Gln Gly Tyr Gln Cys Arg Gln
168 180 185 190
170 Cys Asn Ala Ala Ile His Lys Lys Cys Ile Asp Lys Val Ile Ala Lys
171 195 200 205
173 Cys Thr Gly Ser Ala Ile Asn Ser Arg Glu Thr Met Phe His Lys Glu
174 210 215 220
176 Arg Phe Lys Ile Asp Met Pro His Arg Phe Lys Val Tyr Asn Tyr Lys
177 225 230 235 240
179 Ser Pro Thr Phe Cys Glu His Cys Gly Thr Leu Leu Trp Gly Leu Ala
180 245 250 255
182 Arg Gln Gly Leu Lys Cys Asp Ala Cys Gly Met Asn Val His His Arg
183 260 265 270
185 Cys Gln Thr Lys Val Ala Asn Leu Cys Gly Ile Asn Gln Lys Leu Met
186 275 280 285
188 Ala Glu Ala Leu Ala Met Ile Glu Ser Thr Gln Gln Ala Arg Cys Leu
189 290 295 300
191 Arg Asp Thr Glu Gln Ile Phe Arg Glu Gly Pro Val Glu Ile Gly Leu
192 305 310 315 320
194 Pro Cys Ser Ile Lys Asn Glu Ala Arg Pro Pro Cys Leu Pro Thr Pro
195 325 330 335
197 Gly Lys Arg Glu Pro Gln Gly Ile Ser Trp Glu Ser Pro Leu Asp Glu
198 340 345 350
200 Val Asp Lys Met Cys His Leu Pro Glu Pro Glu Leu Asn Lys Glu Arg
201 355 360 365
203 Pro Ser Leu Gln Ile Lys Leu Lys Ile Glu Asp Phe Ile Leu His Lys
204 370 375 380
206 Met Leu Gly Lys Gly Ser Phe Gly Lys Val Phe Leu Ala Glu Phe Lys
207 385 390 395 400
209 Lys Thr Asn Gln Phe Phe Ala Ile Lys Ala Leu Lys Lys Asp Val Val

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210	405	410	415
212	Leu Met Asp Asp Asp Val Glu Cys Thr Met Val Glu Lys Arg Val Leu		
213	420	425	430
215	Ser Leu Ala Trp Glu His Pro Phe Leu Thr His Met Phe Cys Thr Phe		
216	435	440	445
218	Gln Thr Lys Glu Asn Leu Phe Phe Val Met Glu Tyr Leu Asn Gly Gly		
219	450	455	460
221	Asp Leu Met Tyr His Ile Gln Ser Cys His Lys Phe Asp Leu Ser Arg		
222	465	470	475
224	Ala Thr Phe Tyr Ala Ala Glu Ile Ile Leu Gly Leu Gln Phe Leu His		
225	485	490	495
227	Ser Lys Gly Ile Val Tyr Arg Asp Leu Lys Leu Asp Asn Ile Leu Leu		
228	500	505	510
230	Asp Lys Asp Gly His Ile Lys Ile Ala Asp Phe Gly Met Cys Lys Glu		
231	515	520	525
233	Asn Met Leu Gly Asp Ala Lys Thr Asn Thr Phe Cys Gly Thr Pro Asp		
234	530	535	540
236	Tyr Ile Ala Pro Glu Ile Leu Leu Gly Gln Lys Tyr Asn His Ser Val		
237	545	550	555
239	Asp Trp Trp Ser Phe Gly Val Leu Leu Tyr Glu Met Leu Ile Gly Gln		
240	565	570	575
242	Ser Pro Phe His Gly Gln Asp Glu Glu Glu Leu Phe His Ser Ile Arg		
243	580	585	590
245	Met Asp Asn Pro Phe Tyr Pro Arg Trp Leu Glu Lys Glu Ala Lys Asp		
246	595	600	605
248	Leu Leu Val Lys Leu Phe Val Arg Glu Pro Glu Lys Arg Leu Gly Val		
249	610	615	620
251	Arg Gly Asp Ile Arg Gln His Pro Leu Phe Arg Glu Ile Asn Trp Glu		
252	625	630	635
254	Glu Leu Glu Arg Lys Glu Ile Asp Pro Pro Phe Arg Pro Lys Val Lys		
255	645	650	655
257	Ser Pro Phe Asp Cys Ser Asn Phe Asp Lys Glu Phe Leu Asn Glu Lys		
258	660	665	670
260	Pro Arg Leu Ser Phe Ala Asp Arg Ala Leu Ile Asn Ser Met Asp Gln		
261	675	680	685
263	Asn Met Phe Arg Asn Phe Ser Phe Met Asn Pro Gly Met Glu Arg Leu		
264	690	695	700
266	Ile Ser		
267	705		
270	<210> SEQ ID NO: 10		
271	<211> LENGTH: 706		
272	<212> TYPE: PRT		
273	<213> ORGANISM: Homo sapiens		
275	<400> SEQUENCE: 10		
276	Met Ser Pro Phe Leu Arg Ile Gly Leu Ser Asn Phe Asp Cys Gly Ser		
277	1	5	10
279	Cys Gln Ser Cys Gln Gly Glu Ala Val Asn Pro Tyr Cys Ala Val Leu		
280	20	25	30
282	Val Lys Glu Tyr Val Glu Ser Glu Asn Gly Gln Met Tyr Ile Gln Lys		

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283	35	40	45	
285	Lys Pro Thr Met Tyr Pro Pro Trp Asp Ser Thr Phe Asp Ala His Ile			
286	50	55	60	
288	Asn Lys Gly Arg Val Met Gln Ile Ile Val Lys Gly Lys Asn Val Asp			
289	65	70	75	80
291	Leu Ile Ser Glu Thr Thr Val Glu Leu Tyr Ser Leu Ala Glu Arg Cys			
292	85	90	95	
294	Arg Lys Asn Asn Gly Lys Thr Glu Ile Trp Leu Glu Leu Lys Pro Gln			
295	100	105	110	
297	Gly Arg Met Leu Met Asn Ala Arg Tyr Phe Leu Glu Met Ser Asp Thr			
298	115	120	125	
300	Lys Asp Met Asn Glu Phe Glu Thr Glu Gly Phe Phe Ala Leu His Gln			
301	130	135	140	
303	Arg Arg Gly Ala Ile Lys Gln Ala Lys Val His His Val Lys Cys His			
304	145	150	155	160
306	Glu Phe Thr Ala Thr Phe Phe Pro Gln Pro Thr Phe Cys Ser Val Cys			
307	165	170	175	
309	His Glu Phe Val Trp Gly Leu Asn Lys Gln Gly Tyr Gln Cys Arg Gln			
310	180	185	190	
312	Cys Asn Ala Ala Ile His Lys Lys Cys Ile Asp Lys Val Ile Ala Lys			
313	195	200	205	
315	Cys Thr Gly Ser Ala Ile Asn Ser Arg Glu Thr Met Phe His Lys Glu			
316	210	215	220	
318	Arg Phe Lys Ile Asp Met Pro His Arg Phe Lys Val Tyr Asn Tyr Lys			
319	225	230	235	240
321	Ser Pro Thr Phe Cys Glu His Cys Gly Thr Leu Leu Trp Gly Leu Ala			
322	245	250	255	
324	Arg Gln Gly Leu Lys Cys Asp Ala Cys Gly Met Asn Val His His Arg			
325	260	265	270	
327	Cys Gln Thr Lys Val Ala Asn Leu Cys Gly Ile Asn Gln Lys Leu Met			
328	275	280	285	
330	Ala Glu Ala Leu Ala Met Ile Glu Ser Thr Gln Gln Ala Arg Cys Leu			
331	290	295	300	
333	Arg Asp Thr Glu Gln Ile Phe Arg Glu Gly Pro Val Glu Ile Gly Leu			
334	305	310	315	320
336	Pro Cys Ser Ile Lys Asn Glu Ala Arg Pro Pro Cys Leu Pro Thr Pro			
337	325	330	335	
339	Gly Lys Arg Glu Pro Gln Gly Ile Ser Trp Glu Ser Pro Leu Asp Glu			
340	340	345	350	
342	Val Asp Lys Met Cys His Leu Pro Glu Pro Glu Leu Asn Lys Glu Arg			
343	355	360	365	
345	Pro Ser Leu Gln Ile Lys Leu Lys Ile Glu Asp Phe Ile Leu His Lys			
346	370	375	380	
348	Met Leu Gly Lys Gly Ser Phe Gly Lys Val Phe Leu Ala Glu Phe Lys			
349	385	390	395	400
351	Lys Thr Asn Gln Phe Phe Ala Ile Arg Ala Leu Lys Lys Asp Val Val			
352	405	410	415	
354	Leu Met Asp Asp Asp Val Glu Cys Thr Met Val Glu Lys Arg Val Leu			
355	420	425	430	

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